b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:20.

REMARKS

Claims 1-19 and 22-45 were pending in the application. Claims 1-19 and 22-26 have been cancelled, without prejudice, and new claims 46-49 have been added. Accordingly, after the amendments presented herein have been entered, claims 27-49 will remain pending. For the Examiner's convenience all of the pending claims are set forth herein in Appendix A.

Support for the newly added claims can be found throughout the specification and claims as originally filed. Specifically, support for new claims 46, 47, 48 and 49 can be found in claims 27, 28, 37 and 38 as originally filed, respectively. Further support for newly added claims 46-49 can be found at page 11, lines 10-24, and page 8, lines 35-38 of the specification.

No new matter has been added. Any cancellation of the claims should in no way be construed as an acquiescence to any of the Examiner's rejections and was done solely to expedite the prosecution of the application. Applicant reserves the right to pursue the claims as originally filed in this or a separate application(s).

Withdrawal From Consideration of Claims 28, 30, 32-36, 38, 40, and 42-45 As Being Directed to a Non-Elected Invention

The Examiner has withdrawn claims 28, 30, 38, 40, and claims 32-36 and 42-45 in so far as they depend from any of claims 28, 30, 38, and 40, as being directed toward an invention that is independent or distinct from the invention originally claimed.

Applicant traverses the withdrawal from consideration of these claims for the following reasons. The polypeptide that the Examiner believes is independent from the invention that was originally claimed (SEQ ID NO:20) is a ***splice variant*** of claimed polypeptide (SEQ ID NO:5). Both SEQ ID NO:20 and SEQ ID NO:5 are human capsaicin/vanilloid receptor polypeptides and share a high degree of sequence identity. The two polypeptides are identical with the exception of 164 residues that are deleted in the spice variant (see Figure 17 of the instant application for a

sequence alignment) and share the same structural features. Accordingly, the two polypeptides share a common utility which is based upon shared structural and functional features and, thus, have a unity of invention. Moreover, a search of the full length polypeptide would by default also search the splice variant and, thus, no additional searches that would pose undue burden on the Examiner would be necessary. Therefore, SEQ ID NO:20 is not directed toward an invention that is distinct from the invention originally claimed, and Applicant respectfully requests that the claims directed toward SEQ ID NO:20 be considered and examined by the Examiner.

Rejection of Claims 31-36 and 41-45 Under 35 U.S. C. § 112, First Paragraph

The Examiner has rejected claims 31-36 and 41-45, under 35 U.S.C. § 112, first paragraph because, "the specification, ***while being enabling for the practice of a method of identifying a ligand which binds to a receptor protein comprising the amino acid sequence presented in SEQ ID NO:5 of the instant specification***, does not reasonably provide enablement for the practice of a binding assay which employs a protein having anything less than the entire amino acid sequence presented in SEQ ID NO:5" (***Emphasis added***). The Examiner is further of the opinion that

> [t]he instant specification specifically identifies notable structural features of a protein of the instant invention. It neither provides the identification of the expendable residues in SEQ ID NO:5 nor even a single working example of a functional protein lacking its entire native amino acid sequence.

Applicant traverses this rejection for the following reasons. As indicated in Applicant's previous reply, the teachings in Applicant's specification, and the knowledge generally available in the art at the time of filing would allow a skilled artisan to practice the claimed methods using only routine experimentation.

Contrary to the Examiner's assertions, Applicant has taught in the instant specification which regions of the VR-2 molecules are important for activity and, thus, which regions of the molecule would respond in a binding assay in a manner which is representative of the native protein. Specifically, as taught in the specification (at, for example, page 10, lines 1-35; page 66, lines 30-34; and page 67, lines 1-11), the VR-2 polypeptide contains ankyrin repeats, transmembrane domains, and at least one proline rich domain, all characteristic and necessary for the function of the Capsaicin/Vanilloid family of receptors. Based on these teachings in Applicant's specification, the skilled artisan would be equipped to use a fragment containing one or more of these functional

domains to identify compounds that bind to a domain and modulate an activity of the Capsaicin/Vanilloid receptor. Compounds identified in such a manner would be of practical value, *e.g.*, they could be used as antagonists of a Capsaicin/Vanilloid receptor. For example, as taught in Applicant's specification a fragment of a VR-2 polypeptide containing the proline rich domain may be used by the skilled artisan to identify compounds capable of binding the proline rich domain and disrupting interactions with SH3 domain-containing proteins that act downstream of the VR-2 receptor in a pain signaling pathway. Such a compound would be expected to inhibit the function of the VR-2 polypeptide by disrupting the VR-2 signaling pathway.

Further, contrary to the Examiner's assertion, Applicant does disclose a working example of a fragment of SEQ ID NO:5. SEQ ID NO:20 is a splice variant of SEQ ID NO:5 that is identical in sequence to SEQ ID NO:5 with the exception of a 134 residue deletion from residue 529-663 (see the sequence alignment presented in Figure 17). Moreover, in Example 5 Applicant discloses specific fragments of SEQ ID NO:5 that were used to generate antibodies against human VR2 (see SEQ ID NOs:13, 14 and 15 at page 70 of the specification).

The Examiner further states that, "Applicant has cited a plurality of patent documents in traversal of this rejection. Applicant is advised that none of the patents cited were available at the time the instant application was filed." Applicant respectfully submits that, although the patents submitted were not ***issued*** at the time Applicant filed the instant application, the patents were submitted prior to Applicant's filing date and, thus, ***prove that the methods disclosed therein were common and well known to those of ordinary skill in the art at the time of Applicant's filing***.

With respect to the newly added claims 46-49 which are directed to methods of identifying compounds that modulate polypeptides that are 95% identical to the hVR2 molecules, Applicant would like to point the Examiner's attention to Example 14 *Revised Interim Written Description Guidelines Training Materials.* Example 14 provides that a claim directed to variants of a protein having SEQ ID NO:3 "that are at least 95% identical to SEQ ID NO:3 and catalyze the reaction of A→B" with an accompanying specification that discloses a single species falling within the claimed genus, satisfies the requirements of 35 U.S.C. §112, first paragraph for written description. The rationale behind the foregoing conclusion, as presented by the *Written Description Guidelines*, is that "[t]he single species disclosed is representative of the genus because all members have at least 95% structural identity with the reference compound and because of the presence of an assay which Applicant provided for identifying all of the at least 95% identical variants of SEQ ID NO:3 which are capable of the specified catalytic activity." The Guidelines also provide that "***[t]he procedures***

for making variants of SEQ ID NO:3 are conventional in the art and an assay is described which will identify other proteins having the claimed catalytic activity. Moreover, procedures for making variants of SEQ ID NO:3 which have 95% identity to SEQ ID NO:3 and retain its activity are conventional in the art."

Similarly, in the present case, the claims are directed to methods which use isolated nucleic acid molecules encoding hVR-2 polypeptides comprising an amino acid sequence that is at least 95% identical to the amino acid sequence shown in SEQ ID NOs:5 and 20, wherein the polypeptide is capable of modulating membrane excitability. Furthermore, Applicant has disclosed in the instant specification assays for identifying all of the at least 95% identical variants of SEQ ID NO:5 and 20 which encode polypeptides capable of modulating membrane excitability (see, for example, the patch-clamp methods taught by the Applicant in Example 4). Modulation of membrane excitability is readily testable by one of skill in the art by the methods described in the instant specification and by methods well-known in the relevant art. Accordingly, it would require only routine experimentation on the part of one of skill in the art to mutate the VR-2 molecules of the invention and test them for the ability to modulate membrane excitability as described in the specification.

Based on the foregoing teachings in Applicant's specification and the knowledge generally available in the art at the time of filing, Applicant respectfully submits that the skilled artisan would be able to make and use the claimed invention using only routine experimentation. Accordingly, Applicant respectfully requests that the Examiner reconsider and withdraw the foregoing rejection.

Rejection of Claim 42 Under 35 U.S. C. § 112, First Paragraph

The Examiner has rejected claim 42 under 35 U.S.C. § 112, first paragraph because, "[i]t was well know in the art prior to the time of the instant application that the yeast two-hybrid system can only employ small soluble proteins as shown in Figure 1 of the Chien *et al.* publication." The Examiner is further of the opinion that

> [o]ne of ordinary skill in the art of molecular biology would immediately recognize that a yeast two-hybrid system which employed all of the amino acid sequence of SEQ ID NO:5 would be inoperative because the presence of the six transmembrane domains within that sequence (Figure 1B of Julius *et al.* Pat. No. 6,335,180). In so far as this claim encompasses a system employing only a soluble portion of the amino acid sequence of SEQ ID NO:5, the instant specification does not disclose a practical utility which is to be realized from the identification of a protein which bind[s] to a portion of that amino acid sequence.

Applicant traverses the forgoing rejection for the following reasons. Contrary to the Examiner's assertions, employing fragments of SEQ ID NO:5 in yeast two hybrid assays would be useful in finding modulators that disrupt pain signaling mechanisms. One of ordinary skill in the art would immediately recognize the potential applications of using fragments of a transmembrane protein in screening assays to identify compounds that are capable of binding to an insoluble transmembrane protein. Identification of a compound that binds to a fragment of a transmembrane protein is useful in the modulation of the activity of the protein. For example, a particularly useful application would be the identification of a compound that is capable of binding to an extracellular region of the transmembrane protein and either blocks natural ligand binding, or itself modulates hVR-2 activity in some other manner. Applicant's specification discloses the presence of proline rich domains in hVR-2 polypeptides. Proline rich domains are known to interact with SH3 domains in proteins that act upstream or downstream of hVR-2 in a pain signaling pathway and, thus, the proline rich domains of VR-2 are useful in screening for modulators that disrupt the pain signaling mechanism. Moreover, Applicant's specification provides a hydrophobicity plot for hVR-2 that an ordinary skilled artisan would be able to use to identify those regions of the protein that are on the cell surface. The use of these portions of the protein would allow for the identification of compounds that themselves modulate the activity of the receptor, or through steric effects, abolish the ability of the receptor to bind to other ligands.

Based on the foregoing teachings in Applicant's specification, and the knowledge generally available to one skilled in the art at the time of filing, it is obvious that the ordinary skilled artisan would realize the applications of using fragments of hVR-2 in a two-hybrid system, and would further be able to make and use the claimed invention using only routine experimentation. Accordingly, Applicant respectfully requests that the Examiner reconsider and withdraw the foregoing rejection.

Rejection of Claims 27, 29, 31-34, 36, 37, 39 41, and 43-45 under 35 U.S.C. 102 (e)

The Examiner has rejected claims 27, 29, 31-34, 36, 37, 39 41, and 43-45, under 35 U.S.C. § 102(e) as being anticipated by Julius *et al.* (United States Patent No. 6,335,180 B1). In particular, the Examiner is of the opinion that "[t]he amino acid sequence presented in SEQ ID

NO:5 of the instant application is identical to the amino acid sequence presented in SEQ ID NO:36 of the Julius *et al.* patent."

Applicant respectfully traverses the aforementioned rejection for the following reasons. As evidenced by copies of U.S. Application Serial No: 08/915,461, Provisional Application Serial No: 60/072,151and PCT application Serial No. PCT/US98/17466 (submitted herewith as Appendices B, C, and D, respectively) to which Julius *et al.* claim priority, ***SEQ ID NO:36 is not disclosed in any of these applications***. Accordingly, the 35 U.S.C. § 102(e) date that Julius *et al.* are entitled to with respect to SEQ ID NO:36, is ***January 22, 1999***, the filing date of the Julius *et al.* patent (6,335,180 B1). Moreover, Julius *et al.* disclose ***but do not claim*** the amino acid sequence set forth in SEQ ID NO:36.

Applicant submits herewith a declaration under 37 CFR §1.131 which indicates that Applicant has completed the invention as described and claimed in the above-referenced patent application in this country ***prior to January 22, 1999***. Accordingly, Applicant respectfully submits that the invention disclosed in the present patent application was reduced to practice by the inventor prior to the effective date of the Julius *et al.* reference. As such, the Julius *et al.* reference is not available as prior art against the present invention under 35 U.S.C. 102§(e), and Applicant respectfully requests that the Examiner reconsider and withdraw this rejection.

Rejection of Claim 35 under 35 U.S.C. 103 (a)

The Examiner has rejected claim 35 under 35 U.S.C. § 103(a) as being unpatentable over Julius *et al.* Specifically, the Examiner believes

> [b]ecause the Julius *et al.* patent disclosed the fact that the receptor described therein was naturally expressed in neuronal tissue an artisan would have found it *prima facie* obvious to have expressed that protein recombinantly in a neuronal cell line to obtain a more authentic response by that receptor to a test compound.

Applicant respectfully submits that, in view of the declaration under 37 CFR §1.131 submitted herewith, the aforementioned rejection is rendered moot. Accordingly, Applicant respectfully requests that the Examiner reconsider and withdraw this rejection.

Rejection of Claim 42 under 35 U.S.C. 103 (a)

The Examiner has rejected claim 42 under 35 U.S.C. § 103(a) as being unpatentable over Julius *et al.* in view of Chien *et al.* Specifically, the Examiner believes that

> [t]o have incorporated portions of the capsaicin receptor of Julius *et al.* into the yeast two hybrid system of Chien *et al.* to identify proteins with might interact therewith would have been *prima facie* obvious to one of ordinary skill in the art.

Applicant respectfully submits that, in view of the declaration under 37 CFR §1.131 submitted herewith, the Julius *et al.* patent is not available as prior art against the instant application. The Chien *et al.* publication, by itself, is not sufficient to render claim 42 obvious to one of ordinary skill in the art. Accordingly, Applicant respectfully requests that the Examiner reconsider and withdraw this rejection.

SUMMARY

If a telephone conversation with Applicant's attorney would expedite the prosecution of the above-identified application, the Examiner is urged to call the undersigned at (617) 227-7400.

Respectfully submitted,

LAHIVE & COCKFIELD, LLP

Maria Laccotripe Zacharakis, Ph.D.
Attorney for Applicant
Limited Recognition Under 37 CFR §10.9(b)

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Dated: September 25, 2002

Appendix A

27. A method for identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:5, the method comprising:

a) contacting a cell expressing the polypeptide with a test compound under conditions suitable for binding; and

b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:5.

28. A method for identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:20, the method comprising:

a) contacting a cell expressing the polypeptide with a test compound under conditions suitable for binding; and

b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:20.

29. A method for identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:5, the method comprising:

a) contacting a cell expressing the polypeptide with a test compound under conditions suitable for binding; and

b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:5.

30. A method for identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:20, the method comprising:

a) contacting a cell expressing the polypeptide with a test compound under conditions suitable for binding; and

b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:20.

31. A method for identifying a compound which binds to a polypeptide comprising at least 15 contiguous amino acids of SEQ ID NO:5, the method comprising:

a) contacting a cell expressing the polypeptide with a test compound under conditions suitable binding; and

b) determining whether the test compound binds to said polypeptide, thereby identifying a compound which binds to a polypeptide comprising at least 15 contiguous amino acids of SEQ ID NO:5.

32. The method of any one of claims 27-31, wherein binding of the test compound to the polypeptide is detected by the use of an assay for a hVR-2 activity.

33. The method of claim 32, wherein said hVR-2 activity is modulation of membrane depolarization.

34. The method of claim 32, wherein said hVR-2 activity is modulation of intracellular calcium levels.

35. The method of any one of claims 27-31, wherein said cell expressing said polypeptide is a neuronal cell.

36. The method of any one of claims 27-31 , wherein said compound modulates the activity of said polypeptide.

37. A method for identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:5, the method comprising:

a) contacting a sample comprising the polypeptide with a test compound under conditions suitable for binding; and

b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:5.

38. A method for identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:20, the method comprising:

a) contacting a sample comprising the polypeptide with a test compound under conditions suitable for binding; and

b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:20.

39. A method for identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:5, the method comprising:

a) contacting a sample comprising the polypeptide with a test compound under conditions suitable for binding; and

b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:5.

40. A method for identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:20, the method comprising:

a) contacting a sample comprising the polypeptide with a test compound under conditions suitable for binding; and

b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide consisting of the amino acid sequence of SEQ ID NO:20.

41. A method for identifying a compound which binds to a polypeptide comprising at least 15 contiguous amino acids of SEQ ID NO:5, the method comprising:

a) contacting a sample comprising the polypeptide with a test compound under conditions suitable for binding; and

b) determining whether the test compound binds to said polypeptide, thereby identifying a compound which binds to a polypeptide comprising at least 15 contiguous amino acids of SEQ ID NO:5.

42. The method of any one of claims 27-31 or 37-41, wherein binding of said test compound to said polypeptide is detected by the use of a yeast two-hybrid assay.

43. The method of any one of claims 37-41, wherein binding of said test compound to said polypeptide is detected by the use of a direct binding assay.

44. The method of any one of claims 37-41, wherein binding of said test compound to said polypeptide is detected by the use of a competition binding assay.

45. The method of any one of claims 37-41, wherein said test compound modulates the activity of said polypeptide.

46. A method for identifying a compound which binds to a polypeptide that is 95% identical to the amino acid sequence of SEQ ID NO:5 and is capable of modulating membrane excitability in a cell, the method comprising:

a) contacting a cell expressing the polypeptide with a test compound under conditions suitable for binding; and

b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:5.

47. A method for identifying a compound which binds to a polypeptide that is 95% identical to the amino acid sequence of SEQ ID NO:20 and is capable of modulating membrane excitability in a cell, the method comprising:

a) contacting a cell expressing the polypeptide with a test compound under conditions suitable for binding; and

b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:20.

48. A method for identifying a compound which binds to a polypeptide that is 95% identical to the amino acid sequence of SEQ ID NO:5 and is capable of modulating membrane excitability in a cell, the method comprising:

a) contacting the polypeptide with a test compound under conditions suitable for binding; and

b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:5.

49. A method for identifying a compound which binds to a polypeptide that is 95% identical to the amino acid sequence of SEQ ID NO:20 and is capable of modulating membrane excitability in a cell, the method comprising:

a) contacting the polypeptide with a test compound under conditions suitable for binding; and

b) determining whether the test compound binds to the polypeptide, thereby identifying a compound which binds to a polypeptide comprising the amino acid sequence of SEQ ID NO:20.

Exhibit A

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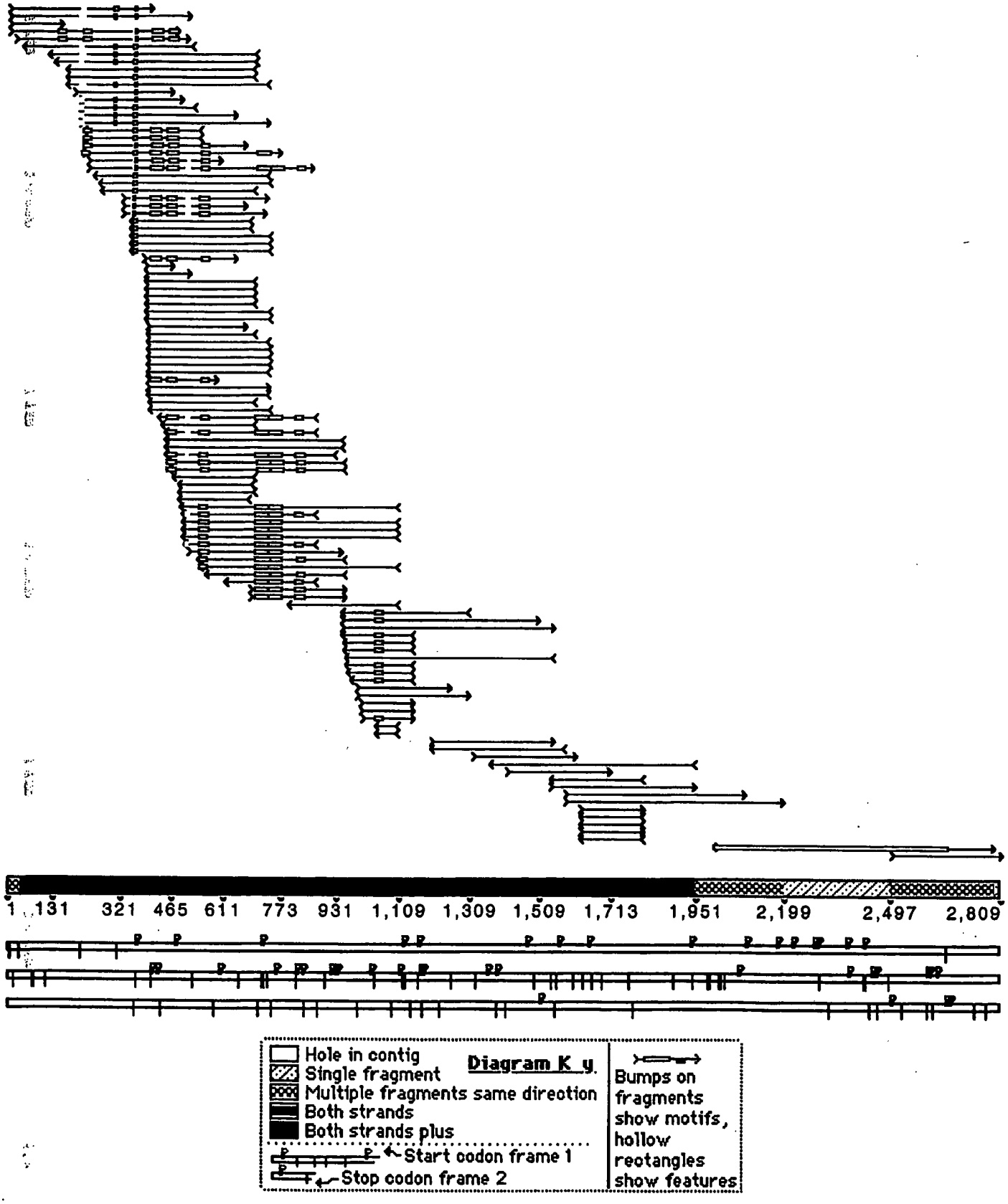

Exhibit B

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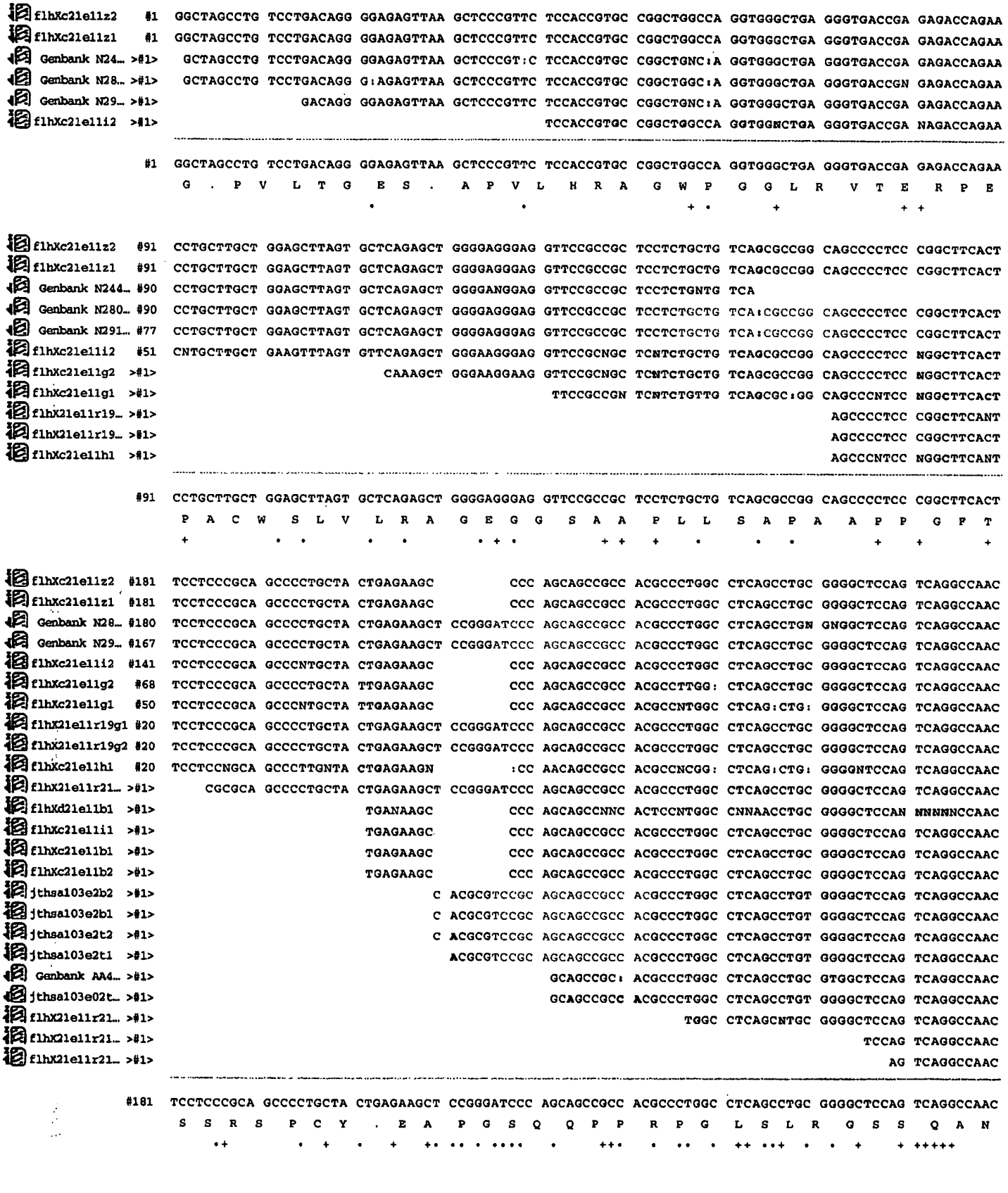

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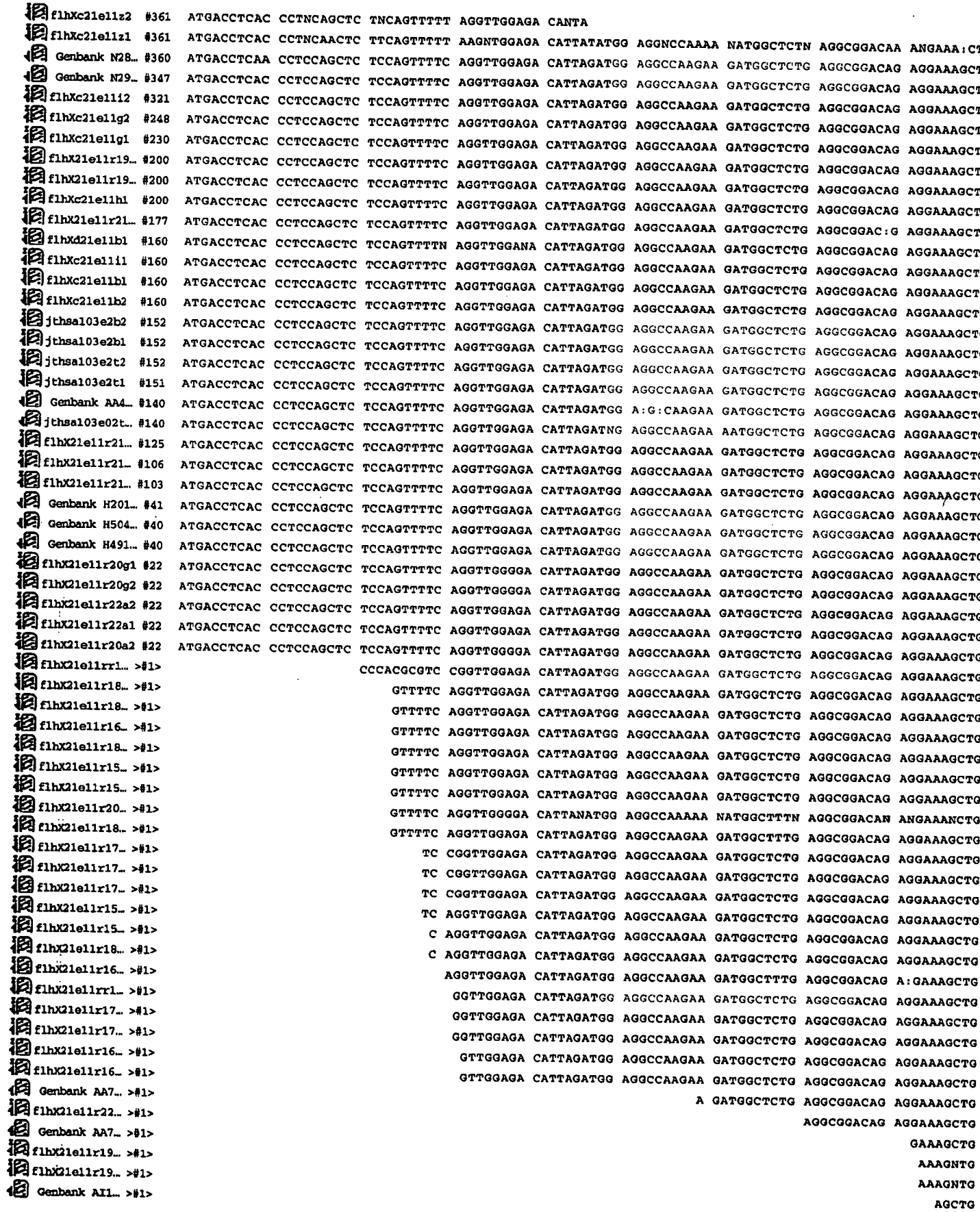

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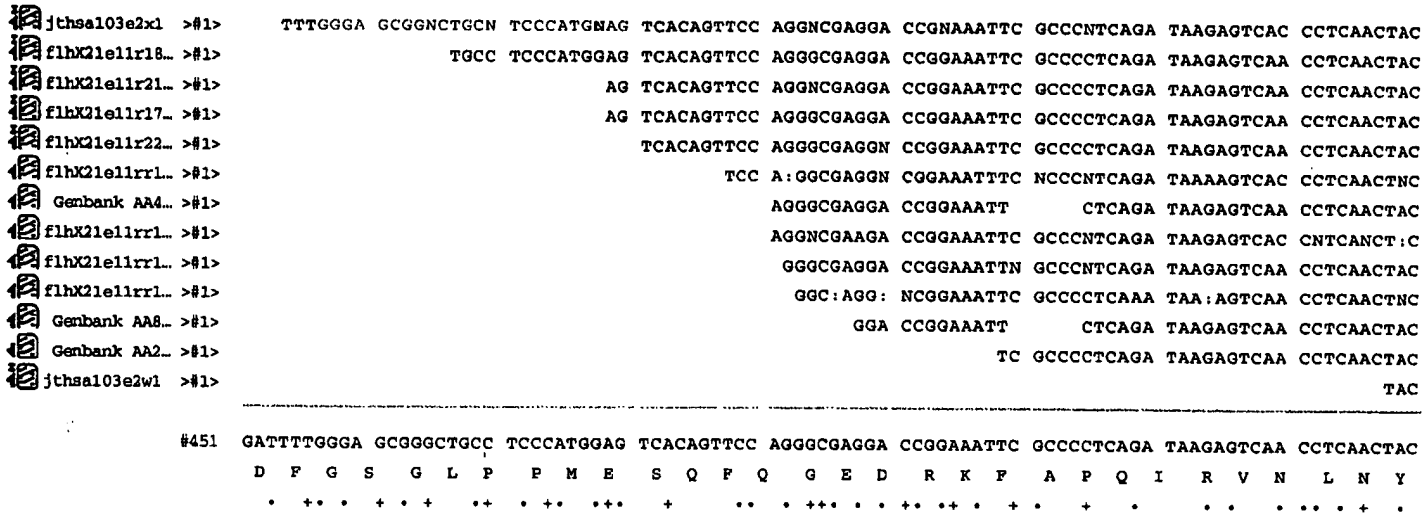

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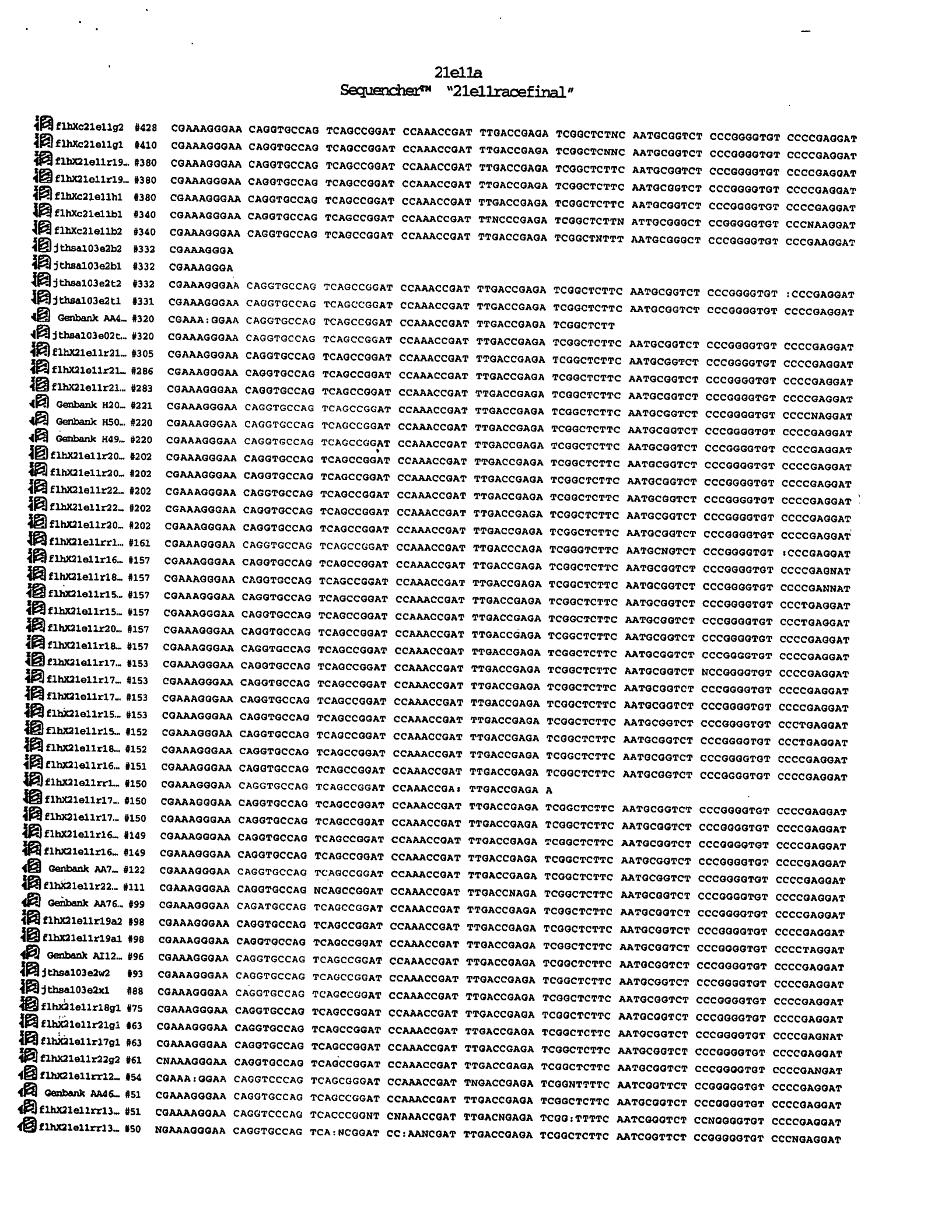

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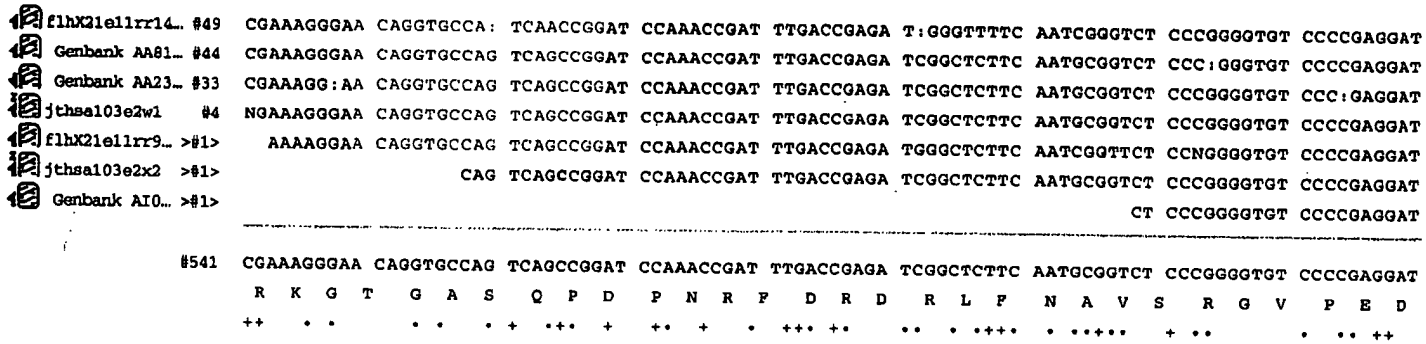

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Sequencher™ "21e11racefinal"

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Sequencher™ "21e11racefinal"

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flhX21e11rr1… #229   ATGAAGGCTG TGCTGAACCT TAAGGACGGG GTCAATGCCT GCATTCTGCC ACTGCTGCAG ATCGACAGGG ACTCTGGCAA TCCTCAGCCC
Genbank AA8…  #224   ATGAAGGCTG TGCTGAACCT TAAGGACGGG GTCAATGCCT GCATTCTGCC ACTGCTGCAG ATCGACAGGG ACTCTGGCAA TCCTCAGCCC
Genbank AA2…  #213   ATGAAGGCTG TGCTGAACCT TAAGGACGGG GTCAATGCCT GCATTCTGCC ACTGCTGCAG ATCGACCGGG ACTCTGGCAA TCCTCAGCCC
jthsa103e2w1  #184   ATGAAGGCTG TGCTGAACCT TAAGGACGGA GTCAATGCCT GCATTCTGCC ACTGCTGCAG ATCGACAGGG ACTCTGGCAA TCCTCAGCCC
flhX21e11rr9… #179   ATGAAGGCTG TGCTGAACCT TAAGGACGGA GTCAATGCCT GCATTCTGTC ACTGCTGCAG ATCGACAGGG ACTCTGGCAA TCCTCAGCCC
jthsa103e2x2  #164   ATGAAGGCTG TGCTGAACCT TAAGGACGGA GTCAATGCCT GCATTCTGCC ACTGCTGCAG ATCGACAGGG ACTCTGGCAA TCCTCAGCCC
Genbank AI0…  #113   ATGAAGGCTG TGCTGAACCT TAAGGACGGG GTCAATGCCT GCATTCTGCC ACTGCTGCAG ATCGACCGGG ACTCTGGCAA TCCTCAGCCC
jthsa103e2a1   #41   ATGAAGGCTG TGCTGAACCT TAAGGACGGA GTCAATGCCT GCATTCTGCC ACTGCTGCAG ATCGACAGGG ACTCTGGCAA TCCTCAGCCC
jthsa103e2a2   #41   ATGAAGGCTG TGCTGAACCT TAAGGACGGA GTCAATGCCT GCATTCTGCC ACTGCTGCAG ATCGACAGGG ACTCTGGCAA TCCTCAGCCC
flhX21e11rr1… >#1>                                                                                    AGGG ACTNTGGCAN TCNTCAGCCC

              #721   ATGAAGGCTG TGCTGAACCT TAAGGACGGA GTCAATGCCT GCATTCTGCC ACTGCTGCAG ATCGACAGGG ACTCTGGCAA TCCTCAGCCC
                      M  K  A  V   L  N  L   K  D  G   V  N  A  C   I  L  P   L  L  Q   I  D  R  D   S  G  N   P  Q  P
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jthsa103e02t... #590   CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGNC ACAGCGC
Genbank AA7... #392    CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATT
Genbank AA7... #369    CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCG:TCT GCACATCGCC ATT
flhX21e11r19... #368   CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATTGAGAAGA GGAGTCTGCA GTGTGTGAAG
flhX21e11r19... #368   CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATTGAGAAGA GGAGTCTGCA GTGTGTGAAG
Genbank AI1... #366    CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATTGAGAAGA GGAGTCTGCA GTGTGTGAAG
jthsa103e2w2  #363     CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATTGAGAAGA GGAGTCTGCA GTGTGTGAAG
jthsa103e2x1  #358     CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATTGAGAAGA GGAGTCTGCA GTGTGTGAAG
flhX21e11rr1... #324   CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGTC ATTGAGAAGA GGAGTCTGCA GTGTGCGAAG
Genbank AA4... #321    CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATT
flhX21e11rr1... #321   CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATTGAGAAGA GGAGTCTGCA GNGTGTNAAG
flhX21e11rr1... #320   CTGGTAAATG CCCAGTGCAC AGATGACTAT TNCCGAGGCC ACAGCGCTCT GCACATCGCC ATTGAGAAGA GGAGTCTGCA GTGTGTGAAG
flhX21e11rr1... #319   CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATTGAGAAGA GGAGTCTGCA GTGTGTGAAG
Genbank AA8... #314    CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATT
Genbank AA2... #303    CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATTGAGAAGA GGAGTCTGCA GTGTGTGAAG
jthsa103e2w1  #274     CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATTGAGAAGA GGAGTCTGCA GTGTGTGAAG
flhX21e11rr9... #269   CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGTC ATTGAGAAGA GGAGTCTGCA GTGTGCGAAG
jthsa103e2x2  #254     CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATTGAGAAGA GGAGTCTGCA GTGTGTGAAG
Genbank AI0... #203    CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATT
jthsa103e2a1  #131     CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATTGAGAAGA GGAGTCTGCA GTGTGTGAAG
jthsa103e2a2  #131     CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATTGAGAAGA GGAGTCTGCA GTGTGTGAAG
flhX21e11rr14... #25   CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATTGAGAAGA GGAGTCTGCA GTGTGTGAAG
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#811   CTGGTAAATG CCCAGTGCAC AGATGACTAT TACCGAGGCC ACAGCGCTCT GCACATCGCC ATTGAGAAGA GGAGTCTGCA GTGTGTGAAG
       L  V  N  A  Q  C  T  D  D  Y  Y  R  G  H  S  A  L  H  I  A  I  E  K  R  S  L  Q  C  V  K
                                     +     +     •     •                       +  •+
```

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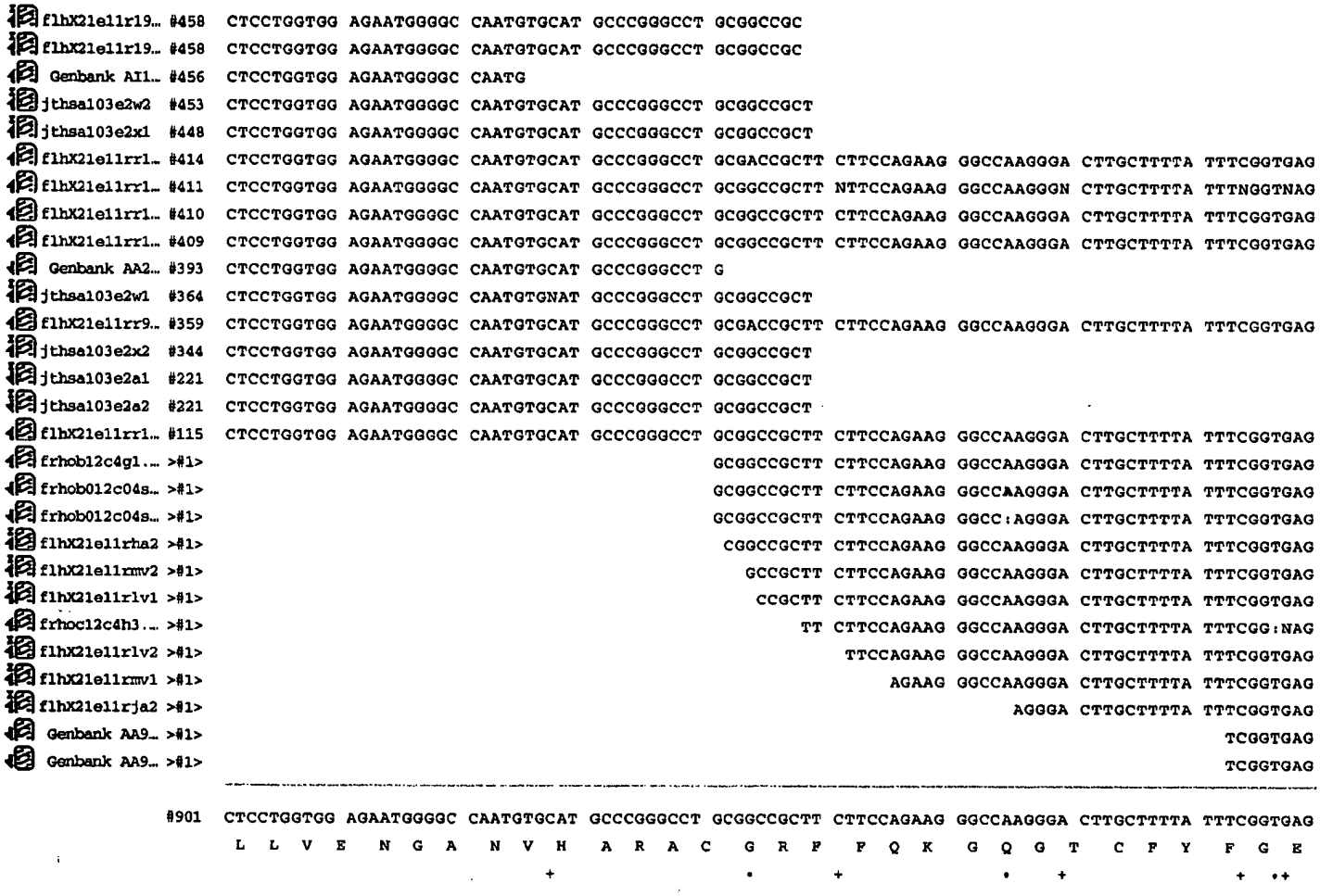

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flhX21e11rr1… #504   CTACCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
flhX21e11rr1… #501   CTACCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCNCCAG CCTGCAGGCC
flhX21e11rr1… #500   CTACCCCTCT CNTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
flhX21e11rr1… #499   CTACCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC GGCCCGCCAG CCTGCAGGCC
flhX21e11rr9… #449   CTACCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
flhX21e11rr1… #205   CTACCCCTCT CTTTGNCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC GGCCCGCCAG CCTGCAGGCC
frhob12c4g1.a… #51   CNACCCCTCT CTTTGNCCGC TTGCACCAAG CAGTGGNATG TGGTAAGCTA CCTCCTGGAG AACCCACNCC AGCCCGCCAG CCTGCAGGCC
frhob012c04s1… #51   CTACCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
frhob012c04s1… #51   CTACCCCTCT CTTTNGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
flhX21e11rha2  #50   CTACCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
flhX21e11rmv2  #48   CTACCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
flhX21e11rlv1  #47   CTACCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
frhoc12c4h3.a… #43   CTACCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCT:GAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
flhX21e11rlv2  #40   CTACCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
flhX21e11rmv1  #36   CTACCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
flhX21e11rja2  #26   CTACCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
Genbank AA992… #9    CTACCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
Genbank AA995… #9    CTACCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
flhX21e11rr9… >#1>      CCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
flhX21e11rr9… >#1>      CCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
jthKb051a01t… >#1>            CTTTGGCCGC TTGCNCCAAG CAGNGGGATG TGGTAAGCTA CCTNCTGGAG AACCCACACC AGNCCGCCAG CCTGCAGGCC
flhX21e11rr1… >#1>                                                        TA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
flhX21e11rr1… >#1>                                                        TA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
```

```
#991   CTACCCCTCT CTTTGGCCGC TTGCACCAAG CAGTGGGATG TGGTAAGCTA CCTCCTGGAG AACCCACACC AGCCCGCCAG CCTGCAGGCC
        L  P  L  S   L  A  A   C  T  K   Q  W  D  V   V  S  Y   L  L  E   N  P  H  Q   P  A  S   L  Q  A
        +           +  ++        +        +  +                 +  •          +   •  +  +
```

```
flhX21e11rr1… #594   ACTGACTCCC AGGGCAACAC AGTC
flhX21e11rr1… #591   ACTGACTCCC AGGGCAACAC NGT
flhX21e11rr1… #590   ACTGACTCCC AGGGCAACAC AGT
flhX21e11rr1… #589   ACTGACTCCC AGGGCAACAC AGTCC
flhX21e11rr9… #539   ACTGACTCCC AGGGCAACAC AGTC
flhX21e11rr1… #295   ACTGACTCCC AGGGCAACAC AGTC
frhob12c4g1.… #141   ANTGACTCCC AGGGCAACAC AGTCCTGCAT GCCCTAGTGA TGATGTCGGN CAANTCAGCT GAGAACATTG CACTGGTGAC CAGCATGTAT
frhob012c04s… #141   ACTGACTCCC AGGGCAACAC AGTCCTGCAT GCCCTAGTGA TGATCTCGGA CAACTCAGCT GAGAACATTG CACTGGTGAC CAGCATGTAT
frhob012c04s… #141   ACTGACTCCC AGGGCAACAC AGTCCTGCAT GCCCTAGTGA TGATCTCGGA CAACTCAGCT GAGAACATTG CACTGGTGAC CAGCATGTAT
flhX21e11rha2 #140   ACTGACTCCC AGGGCAACAC AGTCCTGCAT GCCCTAGTGA TGATCTCGGA CAACTCAGCT GAGAACA
flhX21e11rmv2 #138   ACTGACTCCC AGGGCAACAC AGTCCTGCAT GCCCTAGTGA TGATCTCGGA CAACTCAGCT GAGAACA
flhX21e11rlv1 #137   ACTGACTCCC AGGGCAACAC AGTCCTGCAT GCCCTAGTGA TGATCTCGGA CAACTCAGCT GAGAACA
frhoc12c4h3.… #133   ACTGACTCCC AGGGCAACAC AGTCCTGCAT GCCCTAGTGA TGATCTCGGA CAACTCAGCT GAGAACATTG CACTGGTGAC CAGCATGTAT
flhX21e11rlv2 #130   ACTGACTCCC AGGGCAACAC AGTCCTGCAT GCCCTAGTGA TGATCTCGGA CAACTCAGCT GAGAACA
flhX21e11rmv1 #126   ACTGACTCCC AGGGCAACAC AGTCCTGCAT GCCCTAGTGA TGATGTCGGA CAACTCAGCT GAGAAC
flhX21e11rja2 #116   ACTGACTCCC AGGGCAACAC AGTCCTGCAT GCCCTAGTGA TGATCTCGGA CAACTCAGCT GAGAACA
Genbank AA99… #99    ACTGACTCCC AGGGCAACAC AGTCCTGCAT GCCCTAGTGA TGATCTCGGA CAACTCAGCT GAGAACATTG CACTGGTGAC CAGCATGTAT
Genbank AA99… #99    ACTGACTCCC AGGGCAACAC AGTCCTGCAT GCCCTAGTGA TGATCTCGGA CAACTCAGCT GAGAACATTG CACTGGTGAC CAGCATGTAT
flhX21e11rr9a1 #88   ACTGACTCCC AGGGCAACAC AGTCCTGCAT GCCCTAGTGA TGATCTCGGA CAACTCAGCT GAGAACA
flhX21e11rr9a2 #88   ACTGACTCCC AGGGCAACAC AGTCCTGCAT GCCCTAGTGA TGATCTCGGA CAACTCAGCT GAGAACA
jthKb051a01t1… #81   ACTGACTCCC AGGGCAACAC AGTCCTGCAT GCCCTAGTGA TGATCTCGGA CAACTCAGCT GAGAA
flhX21e11rr11… #43   ACTGACTCCC AGGGCAACAC AGTC
flhX21e11rr11… #43   ACTGACTCCC AGGGCAACAC AGTN
```

```
#1081  ACTGACTCCC AGGGCAACAC AGTCCTGCAT GCCCTAGTGA TGATCTCGGA CAACTCAGCT GAGAACATTG CACTGGTGAC CAGCATGTAT
        T  D  S  Q   G  N  T   V  L  H   A  L  V  M   I  S  D   N  S  A   E  N  I  A   L  V  T   S  M  Y
        +                    +  +                    •     +    +
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frhob12c4g1.…  #231   GATGGGCTCC TCCAAGCTGG GGCCCGCCTC TGCCCTACCG TGCAGCTTGA GGACATCCGC AACCTNCAGG ATCTCACGCC TCTGAAGCTG
frhob012c04s…  #231   GATGGGCTCC TCCAAGCTGG GGCCCGCCTC TGCCCTACCG TGCAGCTTGA GGACATCCGC AACCTGCAGG ATCTCACGCC TCTGAAGCTG
frhob012c04s…  #231   GATGGGCTCC TCCAAGCTGG GGCCCGCCTC TGCCCTACCG TGCAGCTTGA GGACATCCGC AACCTGCAGG ATCTCACGCC TCTGAAGCTG
frhoc12c4h3.…  #223   GATGGGCTCC TCCAAGCTGG GGCCCGCCTC TGCCCTACCG TGCAGCTTGA GGACATCCGC AACCTGCAGG ATCTCACGCC TCTGAAGCTG
Genbank AA9…  #189   GATGGGCTCC TCCAAGCTGG GGCCCGCCTC TGCCCTACCG TGCAGCTTGA GGACATCCGC AACCTGCAGG ATCTCACG
Genbank AA9…  #189   GATGGGCTCC TCCAAGCTGG GGCCCGCCTC TGCCCTACCG TGCAGCTTGA GGACATCCGC AACCTGCAGG ATCTCACGCC TCTGAAGCTG
jthLa029c10t…  >#1>                          CGCCTC TGCCCTACCG TGCAGCTTGA GGACATCCGC AACCTGCAGG ATCTCACGCC TCTGAAGCTG
Genbank W38…  >#1>                            CCTC TGCCCTACCG TGCAGCTTGA GGACATCCGC AACCTGCAGG ATCTCACGCC TCTGAAANTG

#1171  GATGGGCTCC TCCAAGCTGG GGCCCGCCTC TGCCCTACCG TGCAGCTTGA GGACATCCGC AACCTGCAGG ATCTCACGCC TCTGAAGCTG
        D  G  L  L  Q  A  G  A  R  L  C  P  T  V  Q  L  E  D  I  R  N  L  Q  D  L  T  P  L  K  L
                                                                                +                    ++

frhob12c4g1.…  #321   GCCGCCAAGG AGGGCAAGNT CGANATTTTC AGGCACATCC TGCA
frhob012c04s…  #321   GCCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAGCGGGA GTTTTCAGGA CTGAGCCACC TTTCCCGAAA GTTCACCGAG
frhob012c04s…  #321   GCCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAGCGGGA GTTTTCAGGA CTGAGCCACC TTTCCCGAAA GTTCACCGAG
frhoc12c4h3.…  #313   GCCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAGCGGGA GTTTTCAGGA CTGAGCCACC TTTCCCGAAA GTTCACCGAG
Genbank AA9…  #279   GCCGCCAAGG AGGGCAAGAT CGAGATCTTC AGGCACATCC T
jthLa029c10t1…  #67   GCCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAGCGGGA GTTTTCAGGA CTGAGCCACC TTTCCCGAAA GTTCACCGAG
Genbank W386…  #65   GCCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAGCGGGA GTTNTCAGGA CTGAGCCACC TTTCCCGAAA GTTCACCGAG
Genbank AA3…  >#1>                                                                  TTCAGGA CTGAGCCACC TTTCCCGAAA GTTCACCGAG

#1261  GCCGCCAAGG AGGGCAAGAT CGAGATTTTC AGGCACATCC TGCAGCGGGA GTTTTCAGGA CTGAGCCACC TTTCCCGAAA GTTCACCGAG
        A  A  K  E  G  K  I  E  I  F  R  H  I  L  Q  R  E  F  S  G  L  S  H  L  S  R  K  F  T  E
                           +     +  •                        +

frhob012c04s…  #411   TGGTGCTATG GGCCTGTCCG GGTGTCGCTG TATGACCTGG CTTCTGTGGA CAGCTGTGAG GAGAACTCAG TGCTGGAGAT CATTGCCTTT
frhob012c04s…  #411   TGGTGCTATG GGCCTGTCCG GGTGTCGCTG TATGACCT:G CTTCTGTGGA CAGCTGTGAG GAGAACTCAA TGCTGGAGAT CATTGCCTTT
frhoc12c4h3.…  #403   TGGTGCTATG GGCCTGTCCG GGTGTCGCTG TATGACCTGG CTTCTGTGGA CAGCTGTGAG GAGAACTCAG TGCTGGAGAT CATTGCCTTT
jthLa029c10t…  #157   TGGTGCTATG GGCCTGTCCG GGTGTCGCTG TATGACCTGG CTTCTGTGGA CAGCTGTGAG GAGAACTCAG TGCTGGAGAT CATTGCCTTT
Genbank W38…  #155   TGGTGCTATG GGCCTGTCCG GGTGTCGCTG TATGACCTGG CTTCTGTGGA CAGCTGTGAG GAGAACTCAG TGCTGGAGAT CATTGCCTTT
Genbank AA35…  #38   TGGTGCTATG GGCCTGTCCG GGTGTCGCTG TATGACCTGG CTTCTNTGGA CAGCTGTNAG GAGAACTCAG TGCTGGAGAT CATTGCCTTT
frhob12c4c1.…  >#1>            GGCCTGTNCG GGTGTCNCTG TATGACNTGG CTTCTGTGNA CAGCTGTGAN GAGAACTCAG TGCTGGAGAT CATTGCCTTT
Genbank N24…  >#1>                                                                  GAGAACTCAG TGCTGGAGAT CATTGNCTTT

#1351  TGGTGCTATG GGCCTGTCCG GGTGTCGCTG TATGACCTGG CTTCTGTGGA CAGCTGTGAG GAGAACTCAG TGCTGGAGAT CATTGCCTTT
        W  C  Y  G  P  V  R  V  S  L  Y  D  L  A  S  V  D  S  C  E  E  N  S  V  L  E  I  I  A  F
                           +        +        + •      +  +       + +        •              +

frhob012c04s…  #501   CATTGCAAGA GCCCGCACCG ACACCGAATG GTCGNTTTGG AGCCCCTGAA CAAACTGCTG C
frhob012c04s…  #501   CATTGCAAGA ACCCGCACCG ACACCGAATG GTCGNTTTGG AGCCCCTGAA CAAACTGCTG CANGCGAAAT GGGATCTGCT CAT:CCCAAG
frhoc12c4h3.…  #493   CATTGCAAGA GCCCGCACCG ACACCGAATG GTCGTTTTGN AGCCCCTGAA CAAACTGCTG CAGGCGAAAT GGGATCTGCT CATCCCCAAG
jthLa029c10t…  #247   CATTGCAAGA GCCCGNACCG ACACCGAATG GTCGTTTTGG AGCCCCTGAA CAAACTGCTG CANGCGAAAT GGGATCTGCT CATNCNCAAG
Genbank W38…  #245   CATTGCAAGA GCCCGCACCG ACACCGAATG GTCGTTTTGG AGCCCCTGAA CAAACTGCTG CAGGCGAAAT GGGATCTGCT CATCCCCAAG
Genbank AA3…  #128   CATTGCAAGA GCCCGCACCG ACACCGAATG GTCGTTTTGG AGCCCCTGAA CAAACTGCTG CAGGCGAAAT GGGATCTGCT CATCCCCAAG
frhob12c4c1.a…  #81   CATTGCAAGA GNCCGCACCG ACACNGAATG GTCGTTTTGG AGCCCCTGAA CAAACTGCTG CAGNCGAAAT GGGATCTGCT CATCCCCAAG
Genbank N242…  #31   CATTGCAAGA GCCCGNACCG ACACCGAATG GTCGTTTTGG AGCCCCTGAA CAAACTGCTG CAGGCGAAAT GGGATCTGCT CATCCCCAAG

#1441  CATTGCAAGA GCCCGCACCG ACACCGAATG GTCGTTTTGG AGCCCCTGAA CAAACTGCTG CAGGCGAAAT GGGATCTGCT CATCCCCAAG
        H  C  K  S  P  H  R  H  R  M  V  V  L  E  P  L  N  K  L  L  Q  A  K  W  D  L  L  I  P  K
                  •+  +        +        +   +                        ++                    • +
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21e11a

Sequencher™ "21e11racefinal"

```
frhob012c04s… #591   TTCTTCTTAA ACTTCCTG
frhoc12c4h3.… #583   TTCTTCTTAA ACTTCCTG
jthLa029c10t… #337   TTCTTNTTAA ACTTC
Genbank W38… #335    TTCTTCTTAA ACTTCCTGTG TAATCTGATC TACATGTTCA TCTTCA
Genbank AA3… #218    TTCTTCTTAA ACTTCCTGTG TAATCTGATC TACATGTTCA TCTTCAACGC TGTTGCCTAC CATCAGCCTA CCCTGAAGAA G
frhob12c4c1.… #171   TTCTTCTTAA ACTTCCTGTG TAATCTGATN TACATGTTCA TCTTCACCGC TGTTGCCTAC CATCAGCCTA CCCTGAAGAA GCAGGCCGCC
Genbank N24… #121    TTCTTCTTAA ACTTCCTGTG TAATCTGATN TACATGTTCA TCTTCACCGC TGTTGCCTAC CATCAGCCTA CCCTGAAGAA GCAGGCCGCC
flhX21e11aal… >#1>         TTAA ACTTCCTGTG TAATCTGATN TACATGTTCA TCTTCACCGC TGTTGCCTAC CATCAGCCTA CCCTGAAGAA GCAGGCCGCC
frhob12c4e1.… >#1>         TTAA ACTTCCTGTG TAATCTGATC TACATGTTCA TCTTCACCGC TGTTGCCTAC CATCAGCCTA CCCTGAAGAA GCAGGCCGCC
johb003T24ia… >#1>                                                          GC TGTTGCCTAC CATCAGCCTA CCCTGAAGAA G:::GCCGCC
johb003T24ia… >#1>                                                          GC TGTTGCCTAC CATCAGCCTA CCCTGAAGAA G:::GCCGCC
                     ----------------------------------------------------------------------------------------------------

#1531                TTCTTCTTAA ACTTCCTGTG TAATCTGATC TACATGTTCA TCTTCACCGC TGTTGCCTAC CATCAGCCTA CCCTGAAGAA GCAGGCCGCC
                      F  F  L  N   F  L  C   N  L  I   Y  M  F  I   F  T  A   V  A  Y   H  Q  P  T   L  K  K   Q  A  A
                         +                       +                  .                                    ...

frhob12c4c1.… #261   CCTCACCTGA AAGCGGAGGT TGGAAACTCC ATGCTGCTGA CGGGCCACAT CCTTATCCTG CTAGGGGGGA TNTACCTCCT CGTGGGCCAG
Genbank N24… #211    CCTCACCTGA AAGCGGAGGT TGGAAACTCC ATGCTGCTGA CGGGCCACAT CCTTATCCTG CTAGGGGGGA TCTACCTCCT CGTGGG
flhX21e11aal.… #85   CCTCACCTGA AAGCGGAGGT TGGAAACTCC ATGCTGCTGA CGGGCCACAT CCTTATCCTG CTAGGGGGGA TNTACCTCCT CGTGGGCCAG
frhob12c4e1.a… #85   CCTCACCTGA AAGCGGAGGT TGGAAACTCC ATGCTGCTGA CGGGCCACAT CCTTATCCTG CTAGGGGGGA TCTACCTCCT CGTGGGCCAG
johb003T24ia0… #43   CCTCACCTGA AAGCGGAGGT TGGAAACTCC ATGCTGCTGA CGGGCCACAT CCTTATCCTG CTAGGGGGGA TCTACCTCCT CGTGGGCCAG
johb003T24ia0… #43   CCTCACCTGA AAGCGGAGGT TGGAAACTCC ATGCTGCTGA CGGGCCACAT CCTTATCCTG CTAGGGGGGA TCTACCTCCT CGTGGGCCAG
flhX21e11ev2… >#1>     TCACCTGA AAGCGGAGGT TGGAAACTCC ATGCTGCTGA CGGGCCACAT CCTTATCCTG CTAGGGGGGA TCTACCTNCT CGTGGGCCAG
flhX21e11ea2… >#1>     TCACCTGA AAGCGGAGGT TGGAAACTCC ATGCTGCTGA CGGGCCACAT CCTTATCCTG CTAGGGGGGA TNTACCTCCT CGTGGGCCAG
flhX21e11eal… >#1>     TCACCTGA AAGCGNAGGT TGGAAACTCC ANGCTGNTGA CGGGCCACAT CCTTATCCTG CTAGGGGGGA TNTACCTCCT CGTGGNCCAG
flhX21e11dv1… >#1>     TCACCTGA AAGCGGAGGT TGGAAACTCC ATGCTGCTGA CGGGCCACAT CCTTATCCTG CTAGGGGGGA TCTACCTCCT CGTGGGCCAG
flhX21e11da1… >#1>     TCACCTGA AAGNGGAGGT TGGAAACTCC ATGCTGCTGA CGGGCCACAT CCTTATCCTG CTAGGGGGGA TNTACCTCCT CGTGGGCCAG
                     ----------------------------------------------------------------------------------------------------

#1621                CCTCACCTGA AAGCGGAGGT TGGAAACTCC ATGCTGCTGA CGGGCCACAT CCTTATCCTG CTAGGGGGGA TCTACCTCCT CGTGGGCCAG
                      P  H  L  K   A  E  V   G  N  S   M  L  L  T   G  H  I   L  I  L   L  G  G  I   Y  L  L   V  G  Q
                               + +                 +   +                                    +      +         +

frhob12c4c1.… #351   CTGTGGTACT TCTGGCGGCG CCACGTGTTC ATCTGGATCT CGTTCATAGA CAGCTACTTT GAAATCCTCT TCCTGTTCCA GGCCCTGCTC
flhX21e11aal… #175   CTGTGGTACT TCTGGCGGCG CCACGTGTTC ATCTGGATNT CGTTCATAGA CAGCTACTNN GAAATCCTCT TCCTGTTCCA GGCCCTGCTC
frhob12c4e1.… #175   CTGTGGTACT TCTGGCGGCG CCACGTGTTC ATCTGGATCT CGTTCATAGA CAGCTACTTT GAAATCCTCT TCCTGTTCCA GGCCCTGCTC
johb003T24ia… #133   CTGTGGTACT TCTGGCGGCG CCACGTGTTC ATCTGGATCT CGTTCATAGA CAGCTACTTT GAAATCCTCT TCCTGTTCCA GGCCCTGCTC
johb003T24ia… #133   CTGTGGTACT TCTGGCGGCG CCACGTGTTC ATCTGGATCT CGTTCATAGA CAGCTACTTT GAAATCCTCT TCCTGTTCCA GGCCCTGCTC
flhX21e11ev2.… #89   CTGTGGTACT TCTGGCGGNG CCACNTGTTC ATCTGGATCT CGTTCATAGA CAGCTACTTT GAAATCCTCN TCCTGTTNCA NGCCCTGCTC
flhX21e11ea2.… #89   CTGTGGTACT TCTGGCGGCG CCACGTGTTC ATCTGGATCT CGTTCATAGA CAGCTACTTT GAAATCCTCT TCCTGTTCCA GGCCCTGCTC
flhX21e11eal.… #89   CTGTGGTACT TCTGGCGGCG CCACGTGTTC ATCTGGATCT CGTTCATAGA CAGCTACTTT GAAATCCTCT TCCTGTTCCA GGCCCTGCTC
flhX21e11dv1.… #89   CTGTGGTACT TCTGGCGGCG CCACGTGTTC ATCTGGATCT CGTTCATAGA CAGCTACTTT GAAATCCTCT TCCTGTTCCA GGCCCTGCTC
flhX21e11da1.… #89   CTGTGGTACT TCTGGCGGCG CCACGTGTTC ATCTGGATCT CGTTCATAGA CAGCTACTTT GAAATCCTCT TCCTGTTCCA GGCCCTGCTC
                     ----------------------------------------------------------------------------------------------------

#1711                CTGTGGTACT TCTGGCGGCG CCACGTGTTC ATCTGGATCT CGTTCATAGA CAGCTACTTT GAAATCCTCT TCCTGTTCCA GGCCCTGCTC
                      L  W  Y  F   W  R  R   H  V  F   I  W  I  S   F  I  D   S  Y  F   E  I  L  F   L  F  Q   A  L  L
                                     +     +           +                 ++         +       +   +
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21e11a

Sequencher™ "21e11racefinal"

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Achrb21e11 … #425   GGCACTAAGC CAGATGGCAG CCCGGATGAG CGCTGGTGCT TCAGGGTGGA GGAGGTGAAC TGGGCTTCAT GGGAGCAGAC GCTGCCTACG
frhob12c4d1.… >#1>                                                                                  TCAT GGGAGCAGAC GCTGCCTACG

#2431               GGCACTAAGC CAGATGGCAG CCCGGATGAG CGCTGGTGCT TCAGGGTGGA GGAGGTGAAC TGGGCTTCAT GGGAGCAGAC GCTGCCTACG
                     G  T  K  P  D  G  S  P  D  E  R  W  C  F  R  V  E  E  V  N  W  A  S  W  E  Q  T  L  P  T


Achrb21e11 … #515  CTGTGTGAGG ACCCGTCAGG GGCAGGTGTC CCTCGAACTC TCGAGAACCC TGTCCTGGCT TCCCCTCCCA AGGAGGATGA GGATGGTGCC
frhob12c4d1.a… #25  CTGTGTGAGG ACCCGTCAGG GGCAGGTGTC CCTCGAACTC TCGAGNACCC TGTCCTGGCT TCCCCTCCCA AGGAGGATGA GGATGGTGCC

#2521               CTGTGTGAGG ACCCGTCAGG GGCAGGTGTC CCTCGAACTC TCGAGAACCC TGTCCTGGCT TCCCCTCCCA AGGAGGATGA GGATGGTGCC
                     L  C  E  D  P  S  G  A  G  V  P  R  T  L  E  N  P  V  L  A  S  P  P  K  E  D  E  D  G  A
                                                                +

Achrb21e11 … #605   TCTGAGGAAA ACTATGTGCC CGTCCAGCTC CTCCAGTCCA ACTGATGGCC CAGATGCAGC AGGAGGCCAG AGGACAGAGC AGAGGATCTT
frhob12c4d1.… #115  TCTGAGGAAA ACTATGTGCC CGTCCAGCTC CTCCAGTCCA ACTGATGGCC CAGATGCAGC AGGAGGCCAG AGGACAGAGC ANAGGATCTT

#2611               TCTGAGGAAA ACTATGTGCC CGTCCAGCTC CTCCAGTCCA ACTGATGGCC CAGATGCAGC AGGAGGCCAG AGGACAGAGC AGAGGATCTT
                     S  E  E  N  Y  V  P  V  Q  L  L  Q  S  N  .  W  P  R  C  S  R  R  P  E  D  R  A  E  D  L
                                                                                                    +

Achrb21e11 … #695   TCCAACCACA TCTGCTGGCT CTGGGGTCCC AGTGAATTCT GGTGGCAAAT ATATATTTTC ACTAACTCAA AAAAAAAAAA AAAAA
frhob12c4d1.… #205  TCCAACCACA TCTGCTGGCT CTGGGGTCCC AGTGAATTCT GGTGGCAAAT ATATATTTTC ACTAACTCAA AAAAAAAAAA AAAAAAAAAA

#2701               TCCAACCACA TCTGCTGGCT CTGGGGTCCC AGTGAATTCT GGTGGCAAAT ATATATTTTC ACTAACTCAA AAAAAAAAAA AAAAAAAAAA
                     S  N  H  I  C  W  L  W  G  P  S  E  F  W  W  Q  I  Y  I  F  T  N  S  K  K  K  K  K  K  K


frhob12c4d1.… #295  AAAAAAAAAA AAAAAAAAA

#2791               AAAAAAAAAA AAAAAAAAA
                     K  K  K  K  K  K
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